

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER

10 (ii) TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES

15 (iii) NUMBER OF SEQUENCES: 19

20 (iv) CORRESPONDENCE ADDRESS:

25 (A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
Suite 4700

30 (C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 90071

35 (v) COMPUTER READABLE FORM:

40 (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: Word Perfect 5.1

45 (vi) CURRENT APPLICATION DATA:

50 (A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE:
(C) CLASSIFICATION:

55 (vii) PRIOR APPLICATION DATA:

60 Prior applications total,
including application
described below: 1

(viii) ATTORNEY/AGENT INFORMATION:

(ix) TELECOMMUNICATION INFORMATION:

10 (A) TELEPHONE: (619) 552-8400
(B) TELEFAX: (619) 552-0159
(C) TELEX: 67-3510

故其子曰：「吾父之子，其名何也？」

SEQUENCE LISTING

5 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 3517 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Rabbit polyimmunoglobulin receptor

15 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 124....2445

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCCGGGGTT	ACGGGCTGGC	CAGCAGGCTG	TGCCCGAG	TCCGGTCAGCAGGAGGGAA	60	
GAAGTGGCCT	AAAATCTCTC	CCGCATCGGC	AGCCCAGGCC	TAGTGCCCTA	CCAGCCACCA	120
GCC ATG GCT CTC TTC TTG CTC ACC TGC CTG CTG GCT GTC TTT TCA GCG	Met Ala Leu Phe Leu Leu Thr Cys Leu Leu Ala Val Phe Ser Ala					168
1 5 10 15						
30 GCC ACG GCA CAA AGC TCC TTA TTG GGT CCC AGC TCC ATA TTT GGT CCC	Ala Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro					216
20 25 30	20 25 30					
35 GGG GAG GTG AAT GTT TTG GAA GGC GAC TCG GTG TCC ATC ACA TGC TAC	Gly Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr					264
35 40 45	35 40 45					
40 TAC CCA ACA ACC TCC GTC ACC CGG CAC AGC CGG AAG TTC TGG TGC CGG	Tyr Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg					312
40 50 55	50 55 60					
45 GAA GAG GAG AGC GGC CGC TGC GTG ACG CTT GCC TCG ACC GGC TAC ACG	Glu Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr					360
65 70 75	65 70 75					
50 TCC CAG GAA TAC TCC GGG AGA GGC AAG CTC ACC GAC TTC CCT GAT AAA	Ser Gln Glu Tyr Ser Gly Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys					408
80 85 90 95	80 85 90 95					
55 AGC TAC AAG TGT GGC GTG GGA GTC AAC GGC CGT GGC CTG GAC TTC GGT	Ser Tyr Lys Cys Gly Val Gly Val Asn Gly Arg Gly Leu Asp Phe Gly					504
115 120 125	115 120 125					
60 GTC AAC GTG CTG GTC AGC CAG AAG CCA GAG CCT GAT GAC GTT GTT TAC	Val Asn Val Leu Val Ser Gln Lys Pro Glu Pro Asp Asp Val Val Tyr					552
130 135 140	130 135 140					
65 AAA CAA TAT GAG AGT TAT ACA GTA ACC ATC ACC TGC CCT TTC ACA TAT	Lys Gln Tyr Glu Ser Tyr Thr Val Thr Ile Thr Cys Pro Phe Thr Tyr					600
145 150 155	145 150 155					
70 GCG ACT AGG CAA CTA AAG AAG TCC TTT TAC AAG GTG GAA GAC GGG GAA						648

100

	Ala Thr Arg Gln Leu Lys Lys Ser Phe Tyr Lys Val Glu Asp Gly Glu		
160	165	170	175
5	CTT GTA CTC ATC ATT GAT TCC AGC AGT AAG GAG GCA AAG GAC CCC AGG Leu Val Leu Ile Ile Asp Ser Ser Ser Lys Glu Ala Lys Asp Pro Arg		696
	180	185	190
10	TAT AAG GGC AGA ATA ACG TTG CAG ATC CAA AGT ACC ACA GCA AAA GAA Tyr Lys Gly Arg Ile Thr Leu Gln Ile Gln Ser Thr Thr Ala Lys Glu		744
	195	200	205
	TTC ACA GTC ACC ATC AAG CAT TTG CAG CTC AAT GAT GCT GGG CAG TAT Phe Thr Val Thr Ile Lys His Leu Gln Leu Asn Asp Ala Gly Gln Tyr		792
15	210	215	220
	GTC TGC CAG AGT GGA AGC GAC CCC ACT GCT GAA GAA CAG AAC GTT GAC Val Cys Gln Ser Gly Ser Asp Pro Thr Ala Glu Glu Gln Asn Val Asp		840
	225	230	235
20	CTC CGA CTG CTA ACT CCT GGT CTG CTC TAT GGA AAC CTG GGG GGC TCG Leu Arg Leu Leu Thr Pro Gly Leu Leu Tyr Gly Asn Leu Gly Gly Ser		888
	240	245	250
25	255		
	GTG ACC TTT GAA TGT GCC CTG GAC TCT GAA GAC GCA AAC GCG GTA GCA Val Thr Phe Glu Cys Ala Leu Asp Ser Glu Asp Ala Asn Ala Val Ala		936
	260	265	270
	TCC TTG CGC CAG GTT AGG GGT GGC AAT GTG GTC ATT GAC AGC CAG GGG Ser Leu Arg Gln Val Arg Gly Gly Asn Val Val Ile Asp Ser Gln Gly		984
30	275	280	285
	ACA ATA GAT CCA GCC TTC GAG GGC AGG ATC CTG TTC ACC AAG GCT GAG Thr Ile Asp Pro Ala Phe Glu Gly Arg Ile Leu Phe Thr Lys Ala Glu		1032
	290	295	300
35	AAC GGC CAC TTC AGT GTA GTG ATC GCA GGC CTG AGG AAG GAA GAC ACA Asn Gly His Phe Ser Val Val Ile Ala Gly Leu Arg Lys Glu Asp Thr		1080
	305	310	315
40	GGG AAC TAT CTG TGC GGA GTC CAG TCC AAT GGT CAG TCT GGG GAT GGG Gly Asn Tyr Leu Cys Gly Val Gln Ser Asn Gly Gln Ser Gly Asp Gly		1128
	320	325	330
45	335		
	CCC ACC CAG CTT CGG CAA CTC TTC GTC AAT GAA GAG ATC GAC GTG TCC Pro Thr Gln Leu Arg Gln Leu Phe Val Asn Glu Glu Ile Asp Val Ser		1176
	340	345	350
	CGC AGC CCC CCT GTG TTG AAG GGC TTT CCA GGA GGC TCC GTG ACC ATA Arg Ser Pro Pro Val Leu Lys Gly Phe Pro Gly Gly Ser Val Thr Ile		1224
50	355	360	365
	CGC TGC CCC TAC AAC CCG AAG AGA AGC GAC AGC CAC CTG CAG CTG TAT Arg Cys Pro Tyr Asn Pro Lys Arg Ser Asp Ser His Leu Gln Leu Tyr		1272
	370	375	380
55	CTC TGG GAA GGG AGT CAA ACC CGC CAT CTG CTG GTG GAC AGC GGC GAG Leu Trp Glu Gly Ser Gln Thr Arg His Leu Leu Val Asp Ser Gly Glu		1320
	385	390	395
60	Gly Leu Val Gln Lys Asp Tyr Thr Gly Arg Leu Ala Leu Phe Glu Glu 400 405 410 415		1368
	CCT GGC AAT GGC ACC TTC TCA GTC GTC CTC AAC CAG CTC ACT GCC GAG 65 Pro Gly Asn Gly Thr Phe Ser Val Val Leu Asn Gln Leu Thr Ala Glu		1416
	420	425	430

	GAT GAA GGC TTC TAC TGG TGT GTC AGC GAT GAC GAG TCC CTG ACG Asp Glu Gly Phe Tyr Trp Cys Val Ser Asp Asp Asp Glu Ser Leu Thr 435 440 445	1464
5	ACT TCG GTG AAG CTC CAG ATC GTT GAC GGA GAA CCA AGC CCC ACG ATC Thr Ser Val Lys Leu Gln Ile Val Asp Gly Glu Pro Ser Pro Thr Ile 450 455 460	1512
10	GAC AAG TTC ACT GCT GTG CAG GGA GAG CCT GTT GAG ATC ACC TGC CAC Asp Lys Phe Thr Ala Val Gln Gly Glu Pro Val Glu Ile Thr Cys His 465 470 475	1560
15	TTC CCA TGC AAA TAC TTC TCC TCC GAG AAG TAC TGG TGC AAG TGG AAT Phe Pro Cys Lys Tyr Phe Ser Ser Glu Lys Tyr Trp Cys Lys Trp Asn 480 485 490 495	1608
20	GAC CAT GGC TGC GAG GAC CTG CCC ACT AAG CTC AGC TCC AGC GGC GAC Asp His Gly Cys Glu Asp Leu Pro Thr Lys Leu Ser Ser Ser Gly Asp 500 505 510	1656
25	CTT GTG AAA TGC AAC AAC AAC CTG GTC CTC ACC CTG ACC TTG GAC TCG Leu Val Lys Cys Asn Asn Asn Leu Val Leu Thr Leu Thr Leu Asp Ser 515 520 525	1704
30	GTC AGC GAA GAT GAC GAG GGC TGG TAC TGG TGT GGC GCG AAA GAC GGG Val Ser Glu Asp Asp Glu Gly Trp Tyr Trp Cys Gly Ala Lys Asp Gly 530 535 540	1752
35	CAC GAG TTT GAA GAG GTT GCG GCC GTC AGG GTG GAG CTG ACA GAG CCA His Glu Phe Glu Glu Val Ala Ala Val Arg Val Glu Leu Thr Glu Pro 545 550 555	1800
40	GCC AAG GTA GCT GTC GAG CCA GCC AAG GTA CCT GTC GAC CCA GCC AAG Ala Lys Val Ala Val Glu Pro Ala Lys Val Pro Val Asp Pro Ala Lys 560 565 570 575	1848
45	GCA GCC CCC GCG CCT GCT GAG GAG AAG GCC AAG GCG CGG TGC CCA GTG Ala Ala Pro Ala Pro Ala Glu Glu Lys Ala Lys Ala Arg Cys Pro Val 580 585 590	1896
50	CCC AGG AGA AGG CAG TGG TAC CCA TTG TCA AGG AAG CTG AGA ACA AGT Pro Arg Arg Arg Gln Trp Tyr Pro Leu Ser Arg Lys Leu Arg Thr Ser 595 600 605	1944
55	TGT CCA GAA CCT CGG CTC CTT GCG GAG GAG GTA GCA GTG CAG AGT GCG Cys Pro Glu Pro Arg Leu Leu Ala Glu Glu Val Ala Val Gln Ser Ala 610 615 620	1992
60	GAA GAC CCA GCC AGT GGG AGC AGA GCG TCT GTG GAT GCC AGC AGT GCT Glu Asp Pro Ala Ser Gly Ser Arg Ala Ser Val Asp Ala Ser Ser Ala 625 630 635	2040
65	TCG GGA CAA AGC GGG AGT GCC AAA GTA CTG ATC TCC ACC CTG GTG CCC Ser Gly Gln Ser Gly Ser Ala Lys Val Leu Ile Ser Thr Leu Val Pro 640 645 650 655	2088
70	TTG GGG CTG GTG CTG GCA GCG GGG GCC ATG GCC GTG GCC ATA GCC AGA Leu Gly Leu Val Leu Ala Ala Gly Ala Met Ala Val Ala Ile Ala Arg 660 665 670	2136
75	GCC CGG CAC AGG AGG AAC GTG GAC CGA GTT TCC ATC GGA AGC TAC AGG Ala Arg His Arg Arg Asn Val Asp Arg Val Ser Ile Gly Ser Tyr Arg 675 680 685	2184
80	ACA GAC ATT AGC ATG TCA GAC TTG GAG AAC TCC AGG GAG TTC GGA GCC Thr Asp Ile Ser Met Ser Asp Leu Glu Asn Ser Arg Glu Phe Gly Ala	2232

	690	695	700	
5	ATT GAC AAC CCA AGC GCC TGC CCC GAT GCC CGG GAG ACG GCC CTC GGA Ile Asp Asn Pro Ser Ala Cys Pro Asp Ala Arg Glu Thr Ala Leu Gly 705 710 715			2280
10	GGA AAG GAT GAG TTA GCG ACG GCC ACC GAG AGC ACC GTG GAG ATT GAG Gly Lys Asp Glu Leu Ala Thr Ala Thr Glu Ser Thr Val Glu Ile Glu 720 725 730 735			2328
15	GAG CCC AAG AAG GCA AAA CGG TCA TCC AAG GAA GAA GCC GAC CTG GCC Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Ala Asp Leu Ala 740 745 750			2376
20	TAC TCA GCT TTC CTG CTC CAA TCC AAC ACC ATA GCT GCT GAG CAC CAA Tyr Ser Ala Phe Leu Leu Gln Ser Asn Thr Ile Ala Ala Glu His Gln 755 760 765			2424
25	GAT GGC CCC AAG GAG GCC TAG GCACAGCCGG CCACCGCCGC CGCCGCCACC GCCGC Asp Gly Pro Lys Glu Ala 770			2480
30	CGCCGCCGCC ACCTGTGAAA ATCACCTTCC AGAACATCACGT TGATCCTCGG GGTCCCCAGA GCCGGGGCT CAACCGCCCT GCACCCCCCA TGTCCCCACC ACCTAAACTT CCCTACCTGT GCCAGAGGT GTGCTGGTCC CCTCCTCCAC GGATCCAGG CCTGGCTCAA TGTTCCCGTT GGGTGGGGG TGTGAGGGGT TCCTACTTGC AGCCGGTTC TCCCGAGAGA AGCTAAGGAT CCAGGTCTG AGGGAGGGGC CTCTCGAAGG CAGACAGACC AGAGAGGGG GAGGAGCCCT TGGATGGGAG GCCAGAGGGCG CTTTCCGGCC ACCCCCTCCC TCCCTGCCCT CACCCCTCCTT 35		2540	
35	CCTTCATTCA AAAGTCCCAG TGGCTGCTGC CTAGGGTCCA GGCGCTGGCC GCACGCCCTC TCGAAGCCGT TGTGCAAACA TCACTGGAGG AAGCCAGGGC TCCTCCCGGG CTGTGTATCC 40		2600	
40	TCACTCAGGC ATCCTGTCCT CCCCAGTATC AGGAGATGTC AAGCGTCTGA AGGCTGTGTG CCCTGGCGT GTCTGCAAGT CACCCAGAC ACATGTTCTC GCCATTTAC AGATGAGAAC ACTGAGGTTG TACTCAAGGG CACCCCTGCGA GATGGAGCAA CAGCAAACCA GATGGGCTTC 45		2660	
45	TGCTGTCTC TTGGCCAGAG GTCTCTCCAC AGGAGCCCT GCCCCTGTAG GAAGCAGAGT TTTAGAACAT GGAAGAAGAA GAGGGGGATG GCCCTGGACG CTGACCTCTC CCAAGCCCC 50		2720	
50	ACGGGGAAA AGGCCCCCTC CTTTCTGTC ACTCTGGGG ACCTGCGGAG TTGAGCATTG GTGCCCGTG TGTCTGAAGA GTTCCCAGTG GAAAGAAGAA AAGAGGGTGT TTGTCAGTGC CGGGGAGGGC CTGATCCCCA GACAGCTGAA GTTTAAGGTC CTTGTCCCTG TGAGCTTTAA 55		2780	
55	CCAGCACCTC CGGGCTGACC CTTGCTAACCA CATCAGAAAT GTGATTTAAT CATAAACAT TGTGATTGCC ACTGGGA		2840	
60			3080	
65	(2) INFORMATION FOR SEQ ID NO: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 773 amino acids		3140	
			3200	
			3260	
			3320	
			3380	
			3440	
			3500	
			3517	

60

(2) INFORMATION FOR SEQ ID NO: 2:

65 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 773 amino acids

(B) TYPE: amino acid
 (C) STRANNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Rabbit polyimmunoglobulin receptor

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

	Met Ala Leu Phe Leu Leu Thr Cys Leu Leu Ala Val Phe Ser Ala Ala			
1	1	5	10	15
10	Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro Gly			
	20	25	30	
15	Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr Tyr			
	35	40	45	
	Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg Glu			
50	55	60		
20	Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr Ser			
	65	70	75	80
	Gln Glu Tyr Ser Gly Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys Gly			
	85	90	95	
25	Glu Phe Val Val Thr Val Asp Gln Leu Thr Gln Asn Asp Ser Gly Ser			
	100	105	110	
30	Tyr Lys Cys Gly Val Gly Val Asn Gly Arg Gly Leu Asp Phe Gly Val			
	115	120	125	
	Asn Val Leu Val Ser Gln Lys Pro Glu Pro Asp Asp Val Val Tyr Lys			
	130	135	140	
35	Gln Tyr Glu Ser Tyr Thr Val Thr Ile Thr Cys Pro Phe Thr Tyr Ala			
	145	150	155	160
	Thr Arg Gln Leu Lys Lys Ser Phe Tyr Lys Val Glu Asp Gly Glu Leu			
	165	170	175	
40	Val Leu Ile Ile Asp Ser Ser Lys Glu Ala Lys Asp Pro Arg Tyr			
	180	185	190	
45	Lys Gly Arg Ile Thr Leu Gln Ile Gln Ser Thr Thr Ala Lys Glu Phe			
	195	200	205	
	Thr Val Thr Ile Lys His Leu Gln Leu Asn Asp Ala Gly Gln Tyr Val			
	210	215	220	
50	Cys Gln Ser Gly Ser Asp Pro Thr Ala Glu Glu Gln Asn Val Asp Leu			
	225	230	235	240
	Arg Leu Leu Thr Pro Gly Leu Leu Tyr Gly Asn Leu Gly Gly Ser Val			
	245	250	255	
55	Thr Phe Glu Cys Ala Leu Asp Ser Glu Asp Ala Asn Ala Val Ala Ser			
	260	265	270	
	Leu Arg Gln Val Arg Gly Gly Asn Val Val Ile Asp Ser Gln Gly Thr			
60	275	280	285	
	Ile Asp Pro Ala Phe Glu Gly Arg Ile Leu Phe Thr Lys Ala Glu Asn			
	290	295	300	
65	Gly His Phe Ser Val Val Ile Ala Gly Leu Arg Lys Glu Asp Thr Gly			
	305	310	315	320

	Asn Tyr Leu Cys Gly Val Gln Ser Asn Gly Gln Ser Gly Asp Gly Pro			
	325	330	335	
5	Thr Gln Leu Arg Gln Leu Phe Val Asn Glu Glu Ile Asp Val Ser Arg			
	340	345	350	
	Ser Pro Pro Val Leu Lys Gly Phe Pro Gly Gly Ser Val Thr Ile Arg			
	355	360	365	
10	Cys Pro Tyr Asn Pro Lys Arg Ser Asp Ser His Leu Gln Leu Tyr Leu			
	370	375	380	
	Trp Glu Gly Ser Gln Thr Arg His Leu Leu Val Asp Ser Gly Glu Gly			
15	385	390	395	400
	Leu Val Gln Lys Asp Tyr Thr Gly Arg Leu Ala Leu Phe Glu Glu Pro			
	405	410	415	
20	Gly Asn Gly Thr Phe Ser Val Val Leu Asn Gln Leu Thr Ala Glu Asp			
	420	425	430	
	Glu Gly Phe Tyr Trp Cys Val Ser Asp Asp Asp Glu Ser Leu Thr Thr			
	435	440	445	
25	Ser Val Lys Leu Gln Ile Val Asp Gly Glu Pro Ser Pro Thr Ile Asp			
	450	455	460	
	Lys Phe Thr Ala Val Gln Gly Glu Pro Val Glu Ile Thr Cys His Phe			
30	465	470	475	480
	Pro Cys Lys Tyr Phe Ser Ser Glu Lys Tyr Trp Cys Lys Trp Asn Asp			
	485	490	495	
35	His Gly Cys Glu Asp Leu Pro Thr Lys Leu Ser Ser Ser Gly Asp Leu			
	500	505	510	
	Val Lys Cys Asn Asn Leu Val Leu Thr Leu Thr Leu Asp Ser Val			
	515	520	525	
40	Ser Glu Asp Asp Glu Gly Trp Tyr Trp Cys Gly Ala Lys Asp Gly His			
	530	535	540	
	Glu Phe Glu Glu Val Ala Ala Val Arg Val Glu Leu Thr Glu Pro Ala			
45	545	550	555	560
	Lys Val Ala Val Glu Pro Ala Lys Val Pro Val Asp Pro Ala Lys Ala			
	565	570	575	
50	Ala Pro Ala Pro Ala Glu Glu Lys Ala Lys Ala Arg Cys Pro Val Pro			
	580	585	590	
	Arg Arg Arg Gln Trp Tyr Pro Leu Ser Arg Lys Leu Arg Thr Ser Cys			
	595	600	605	
55	Pro Glu Pro Arg Leu Leu Ala Glu Glu Val Ala Val Gln Ser Ala Glu			
	610	615	620	
	Asp Pro Ala Ser Gly Ser Arg Ala Ser Val Asp Ala Ser Ser Ala Ser			
60	625	630	635	640
	Gly Gln Ser Gly Ser Ala Lys Val Leu Ile Ser Thr Leu Val Pro Leu			
	645	650	655	
65	Gly Leu Val Leu Ala Ala Gly Ala Met Ala Val Ala Ile Ala Arg Ala			
	660	665	670	

Arg His Arg Arg Asn Val Asp Arg Val Ser Ile Gly Ser Tyr Arg Thr
 675 680 685
 5 Asp Ile Ser Met Ser Asp Leu Glu Asn Ser Arg Glu Phe Gly Ala Ile
 690 695 700
 Asp Asn Pro Ser Ala Cys Pro Asp Ala Arg Glu Thr Ala Leu Gly Gly
 705 710 715 720
 10 Lys Asp Glu Leu Ala Thr Ala Thr Glu Ser Thr Val Glu Ile Glu Glu
 725 730 735
 Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Leu Ala Tyr
 15 740 745 750
 Ser Ala Phe Leu Leu Gln Ser Asn Thr Ile Ala Ala Glu His Gln Asp
 755 760 765
 20 Gly Pro Lys Glu Ala
 770

25 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 2919 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Human polyimmunoglobulin Receptor

35 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 235....2472

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AGAGTTTCAG TTTTGGCAGC AGCGTCCAGT GCCCTGCCAG TAGCTCCTAG AGAGGCAGGG	60
GTTACCAACT GGCCAGCAGG CTGTGTCCCT GAAGTCAGAT CAACGGGAGA GAAGGAAGTG	120
45 GCTAAAACAT TGCACACAGGAG AAGTCGGCCT GAGTGGTGCG GCGCTCGGGA CCCACCAGCA	180
ATGCTGCTCT TCGTGCTCAC CTGCCTGCTG GCGGTCTTCC CAGCCATCTC CACG AAG	237
50 Lys 1	
AGT CCC ATA TTT GGT CCC GAG GAG GTG AAT AGT GTG GAA GGT AAC TCA	285
Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu Gly Asn Ser	
5 10 15	
55 GTG TCC ATC ACG TGC TAC TAC CCA CCC ACC TCT GTC AAC CGG CAC ACC	333
Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His Thr	
20 25 30	
60 CGG AAG TAC TGG TGC CGG CAG GGA GCT AGA GGT GGC TGC ATA ACC CTC	381
Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys Ile Thr Leu	
35 40 45	
65 ATC TCC TCG GAG GGC TAC GTC TCC AGC AAA TAT GCA GGC AGG GCT AAC	429
Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys Tyr Ala Gly Arg Ala Asn	
50 55 60 65	

	CTC ACC AAC TTC CCG GAG AAC GGC ACA TTT GTG GTG AAC ATT GCC CAG Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn Ile Ala Gln 70 75 80	477
5	CTG AGC CAG GAT GAC TCC GGG CGC TAC AAG TGT GGC CTG GGC ATC AAT Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile Asn 85 90 95	525
10	AGC CGA GGC CTG TCC TTT GAT GTC AGC CTG GAG GTC AGC CAG GGT CCT Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser Gln Gly Pro 100 105 110	573
15	GGG CTC CTA AAT GAC ACT AAA GTC TAC ACA GTG GAC CTG GGC AGA ACG Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu Gly Arg Thr 115 120 125	621
20	GTG ACC ATC AAC TGC CCT TTC AAG ACT GAG AAT GCT CAA AAG AGG AAG Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln Lys Arg Lys 130 135 140 145	669
25	TCC TTG TAC AAG CAG ATA GGC CTG TAC CCT GTG CTG GTC ATC GAC TCC Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val Ile Asp Ser 150 155 160	717
30	AGT GGT TAT GTG AAT CCC AAC TAT ACA GGA AGA ATA CGC CTT GAT ATT Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg Leu Asp Ile 165 170 175	765
35	CAG GGT ACT GGC CAG TTA CTG TTC AGC GTT GTC ATC AAC CAA CTC AGG Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn Gln Leu Arg 180 185 190	813
40	CTC AGC GAT GCT GGG CAG TAT CTC TGC CAG GCT GGG GAT GAT TCC AAT Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp Asp Ser Asn 195 200 205	861
45	AGT AAT AAG AAG AAT GCT GAC CTC CAA GTG CTA AAG CCC GAG CCC GAG Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro Glu Pro Glu 210 215 220 225	909
50	CTG GTT TAT GAA GAC CTG AGG GGC TCA GTG ACC TTC CAC TGT GCC CTG Leu Val Tyr Glu Asp Leu Arg Gly Ser Val Thr Phe His Cys Ala Leu 230 235 240	957
55	GGC CCT GAG GTG GCA AAC GTG GCC AAA TTT CTG TGC CGA CAG AGC AGT Gly Pro Glu Val Ala Asn Val Ala Lys Phe Leu Cys Arg Gln Ser Ser 245 250 255	1005
60	GGG GAA AAC TGT GAC GTG GTC GTC AAC ACC CTG GGG AAG AGG GCC CCA Gly Glu Asn Cys Asp Val Val Val Asn Thr Leu Gly Lys Arg Ala Pro 260 265 270	1053
65	GCC TTT GAG GGC AGG ATC CTG CTC AAC CCC CAG GAC AAG GAT GGC TCA Ala Phe Glu Gly Arg Ile Leu Leu Asn Pro Gln Asp Lys Asp Gly Ser 275 280 285	1101
70	TTC AGT GTG GTG ATC ACA GGC CTG AGG AAG GAG GAT GCA GGG CGC TAC Phe Ser Val Val Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly Arg Tyr 290 295 300 305	1149
75	CTG TGT GGA GCC CAT TCG GAT GGT CAG CTG CAG GAA GGC TCG CCT ATC Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly Ser Pro Ile 310 315 320	1197
80	CAG GCC TGG CAA CTC TTC GTC AAT GAG GAG TCC ACG ATT CCC CGC AGC Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro Arg Ser	1245

	325	330	335	
5	CCC ACT GTG GTG AAG GGG GTG GCA GGA AGC TCT GTG CCC GTG CTC TGC Pro Thr Val Val Lys Gly Val Ala Gly Ser Ser Val Ala Val Leu Cys 340 345 350			1293
	CCC TAC AAC CGT AAG GAA AGC AAA AGC ATC AAG TAC TGG TGT CTC TGG Pro Tyr Asn Arg Lys Glu Ser Lys Ser Ile Lys Tyr Trp Cys Leu Trp 355 360 365			1341
10	GAA GGG GCC CAG AAT GGC CGC TGC CCC CTG CTG GTG GAC AGC GAG GGG Glu Gly Ala Gln Asn Gly Arg Cys Pro Leu Leu Val Asp Ser Glu Gly 370 375 380 385			1389
15	TGG GTT AAG GCC CAG TAC GAG GGC CGC CTC TCC CTG CTG GAG GAG CCA Trp Val Lys Ala Gln Tyr Glu Gly Arg Leu Ser Leu Leu Glu Glu Pro 390 395 400			1437
20	GGC AAC GGC ACC TTC ACT GTC ATC CTC AAC CAG CTC ACC AGC CGG GAC Gly Asn Gly Thr Phe Thr Val Ile Leu Asn Gln Leu Thr Ser Arg Asp 405 410 415			1485
25	GCC GGC TTC TAC TGG TGT CTG ACC AAC GGC GAT ACT CTC TGG AGG ACC Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Thr Leu Trp Arg Thr 420 425 430			1533
	ACC GTG GAG ATC AAG ATT ATC GAA GGA GAA CCA AAC CTC AAG GTA CCA Thr Val Glu Ile Lys Ile Ile Glu Gly Glu Pro Asn Leu Lys Val Pro 435 440 445			1581
30	GGG AAT GTC ACG GCT GTG CTG GGA GAG ACT CTC AAG GTC CCC TGT CAC Gly Asn Val Thr Ala Val Leu Gly Glu Thr Leu Lys Val Pro Cys His 450 455 460 465			1629
35	TTT CCA TGC AAA TTC TCC TCG TAC GAG AAA TAC TGG TGC AAG TGG AAT Phe Pro Cys Lys Phe Ser Ser Tyr Glu Lys Tyr Trp Cys Lys Trp Asn 470 475 480			1677
40	AAC ACG GGC TGC CAG GCC CTG CCC AGC CAA GAC GAA GGC CCC AGC AAG Asn Thr Gly Cys Gln Ala Leu Pro Ser Gln Asp Glu Gly Pro Ser Lys 485 490 495			1725
45	GCC TTC GTG AAC TGT GAC GAG AAC AGC CGG CTT GTC TCC CTG ACC CTG Ala Phe Val Asn Cys Asp Glu Asn Ser Arg Leu Val Ser Leu Thr Leu 500 505 510			1773
	AAC CTG GTG ACC AGG GCT GAT GAG GGC TGG TAC TGG TGT GGA GTG AAG Asn Leu Val Thr Arg Ala Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys 515 520 525			1821
50	CAG GGC CAC TTC TAT GGA GAG ACT GCA GCC GTC TAT GTG GCA GTT GAA Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala Val Glu 530 535 540 545			1869
55	GAG AGG AAG GCA GCG GGG TCC CGC GAT GTC AGC CTA GCG AAG GCA GAC Glu Arg Lys Ala Ala Gly Ser Arg Asp Val Ser Leu Ala Lys Ala Asp 550 555 560			1917
60	GCT GCT CCT GAT GAG AAG GTG CTA GAC TCT GGT TTT CGG GAG ATT GAG Ala Ala Pro Asp Glu Lys Val Leu Asp Ser Gly Phe Arg Glu Ile Glu 565 570 575			1965
	AAC AAA GCC ATT CAG GAT CCC AGG CTT TTT GCA GAG GAA AAG GCG GTG Asn Lys Ala Ile Gln Asp Pro Arg Leu Phe Ala Glu Glu Lys Ala Val 580 585 590			2013
65				

	GCA GAT ACA AGA GAT CAA GCC GAT GGG AGC AGA GCA TCT GTG GAT TCC Ala Asp Thr Arg Asp Gln Ala Asp Gly Ser Arg Ala Ser Val Asp Ser 595 600 605	2061
5	GGC AGC TCT GAG GAA CAA GGT GGA AGC TCC AGA GCG CTG GTC TCC ACC Gly Ser Ser Glu Glu Gln Gly Ser Ser Arg Ala Leu Val Ser Thr 610 615 620 625	2109
10	CTG GTG CCC CTG GGC CTG GTG CTG GCA GTG GGA GCC GTG GCT GTG GGG Leu Val Pro Leu Gly Leu Val Leu Ala Val Gly Ala Val Ala Val Gly 630 635 640	2157
15	GTG GCC AGA GCC CGG CAC AGG AAG AAC GTC GAC CGA GTT TCA ATC AGA Val Ala Arg Ala Arg His Arg Lys Asn Val Asp Arg Val Ser Ile Arg 645 650 655	2205
20	AGC TAC AGG ACA GAC ATT AGC ATG TCA GAC TTC GAG AAC TCC AGG GAA Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu Asn Ser Arg Glu 660 665 670	2253
25	TTT GGA GCC AAT GAC AAC ATG GGA GCC TCT TCG ATC ACT CAG GAG ACA Phe Gly Ala Asn Asp Asn Met Gly Ala Ser Ser Ile Thr Gln Glu Thr 675 680 685	2301
30	TCC CTC GGA GGA AAA GAA GAG TTT GTT GCC ACC ACT GAG AGC ACC ACA Ser Leu Gly Gly Lys Glu Glu Phe Val Ala Thr Thr Glu Ser Thr Thr 690 695 700 705	2349
35	GAG ACC AAA GAA CCC AAG AAG GCA AAA AGG TCA TCC AAG GAG GAA GCC Glu Thr Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala 710 715 720	2397
40	GAG ATG GCC TAC AAA GAC TTC CTG CTC CAG TCC AGC ACC GTG GCC GCC Glu Met Ala Tyr Lys Asp Phe Leu Leu Gln Ser Ser Thr Val Ala Ala 725 730 735	2445
45	GAG GCC CAG GAC GGC CCC CAG GAA GCC TAGACGGTGT CGCCGCCTGC TCCCTGCA Glu Ala Gln Asp Gly Pro Gln Glu Ala 740 745	2500
50	CCCATGACAA TCACCTTCAG AATCATGTCTG ATCCTGGGGG CCCTCAGCTC CTGGGGACCC CACTCCCTGC TCTAACACCT GCCTAGGTTT TTCCCTACTGT CCTCAGAGGC GTGCTGGTCC GCTCCTCAGT GACATCAAAG CCTGGCCTAA TTGTTCTAT TGGGGATGAG GGTGGCATGA GGAGGTCCA CTTGCAACTT CTTCTGTTG AGAGAACCTC AGGTACGGAG AAGAATAGAG GTCCTCATGG GTCCCTTGAA GGAAGAGGGA CCAGGGTGGG AGAGCTGATT GCAGAAAGGA GAGACGTGCA GCGCCCCCTCT GCACCCCTTAT CATGGGATGT CAACAGAATT TTTTCCCTCC ACTCCATCCC TCCCTCCCGT CCTTCCCCTC TTCTTCTTTC CTTACCATCA AAAGATGTA	2560 2620 2680 2740 2800 2860 2919
55		

(2) INFORMATION FOR SEQ ID NO: 4:

60	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 746 amino acids
	(B) TYPE: amino acid
	(C) STRANNESS: single
65	(D) TOPOLOGY: linear
	DESCRIPTION: Human Polyimmunoglobulin Receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu Gly Asn
 1 5 10 15

5 Ser Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His
 20 25 30

10 Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys Ile Thr
 35 40 45

Leu Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys Tyr Ala Gly Arg Ala
 50 55 60

15 Asn Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn Ile Ala
 65 70 75 80

Gln Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile
 85 90 95

20 Asn Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser Gln Gly
 100 105 110

25 Pro Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu Gly Arg
 115 120 125

Thr Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln Lys Arg
 130 135 140

30 Lys Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val Ile Asp
 145 150 155 160

Ser Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg Leu Asp
 165 170 175

35 Ile Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn Gln Leu
 180 185 190

Arg Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp Asp Ser
 195 200 205

40 Asn Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro Glu Pro
 210 215 220

45 Glu Leu Val Tyr Glu Asp Leu Arg Gly Ser Val Thr Phe His Cys Ala
 225 230 235 240

Leu Gly Pro Glu Val Ala Asn Val Ala Lys Phe Leu Cys Arg Gln Ser
 245 250 255

50 Ser Gly Glu Asn Cys Asp Val Val Val Asn Thr Leu Gly Lys Arg Ala
 260 265 270

55 Pro Ala Phe Glu Gly Arg Ile Leu Leu Asn Pro Gln Asp Lys Asp Gly
 275 280 285

Ser Phe Ser Val Val Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly Arg
 290 295 300

60 Tyr Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly Ser Pro
 305 310 315 320

Ile Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro Arg
 325 330 335

65 Ser Pro Thr Val Val Lys Gly Val Ala Gly Ser Ser Val Ala Val Leu

	340	345	350	
	Cys Pro Tyr Asn Arg Lys Glu Ser Lys Ser Ile Lys Tyr Trp Cys Leu			
	355	360	365	
5	Trp Glu Gly Ala Gln Asn Gly Arg Cys Pro Leu Leu Val Asp Ser Glu			
	370	375	380	
	Gly Trp Val Lys Ala Gln Tyr Glu Gly Arg Leu Ser Leu Leu Glu Glu			
10	385	390	395	400
	Pro Gly Asn Gly Thr Phe Thr Val Ile Leu Asn Gln Leu Thr Ser Arg			
	405	410	415	
15	Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Thr Leu Trp Arg			
	420	425	430	
	Thr Thr Val Glu Ile Lys Ile Ile Glu Gly Glu Pro Asn Leu Lys Val			
	435	440	445	
20	Pro Gly Asn Val Thr Ala Val Leu Gly Glu Thr Leu Lys Val Pro Cys			
	450	455	460	
	His Phe Pro Cys Lys Phe Ser Ser Tyr Glu Lys Tyr Trp Cys Lys Trp			
25	465	470	475	480
	Asn Asn Thr Gly Cys Gln Ala Leu Pro Ser Gln Asp Glu Gly Pro Ser			
	485	490	495	
30	Lys Ala Phe Val Asn Cys Asp Glu Asn Ser Arg Leu Val Ser Leu Thr			
	500	505	510	
	Leu Asn Leu Val Thr Arg Ala Asp Glu Gly Trp Tyr Trp Cys Gly Val			
	515	520	525	
35	Lys Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala Val			
	530	535	540	
	Glu Glu Arg Lys Ala Ala Gly Ser Arg Asp Val Ser Leu Ala Lys Ala			
40	545	550	555	560
	Asp Ala Ala Pro Asp Glu Lys Val Leu Asp Ser Gly Phe Arg Glu Ile			
	565	570	575	
45	Glu Asn Lys Ala Ile Gln Asp Pro Arg Leu Phe Ala Glu Glu Lys Ala			
	580	585	590	
	Val Ala Asp Thr Arg Asp Gln Ala Asp Gly Ser Arg Ala Ser Val Asp			
	595	600	605	
50	Ser Gly Ser Ser Glu Glu Gln Gly Ser Ser Arg Ala Leu Val Ser			
	610	615	620	
	Thr Leu Val Pro Leu Gly Leu Val Leu Ala Val Gly Ala Val Ala Val			
55	625	630	635	640
	Gly Val Ala Arg Ala Arg His Arg Lys Asn Val Asp Arg Val Ser Ile			
	645	650	655	
60	Arg Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu Asn Ser Arg			
	660	665	670	
	Glu Phe Gly Ala Asn Asp Asn Met Gly Ala Ser Ser Ile Thr Gln Glu			
	675	680	685	
65	Thr Ser Leu Gly Gly Lys Glu Glu Phe Val Ala Thr Thr Glu Ser Thr			

690	695	700
5	Thr Glu Thr Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu 705 710 715 720	
	Ala Glu Met Ala Tyr Lys Asp Phe Leu Leu Gln Ser Ser Thr Val Ala 725 730 735	
10	Ala Glu Ala Gln Asp Gly Pro Gln Glu Ala 740 745	

15 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 3630 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	DESCRIPTION: Bovine Polyimmunoglobulin Receptor

25 (ix) FEATURE:

25	(A) NAME/KEY: Coding Sequence
	(B) LOCATION: 152....2425

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

30	GATCTCCTCG GAGGGTCGTG CAGCGGCCCT GGGTCCCTGC CGGCACCAAGT ACTTGCGCGT 60	
	GTGCTCCCAA AGCTGACGGG ATAGGAGGAA GGAGCTAAA CAACCACACA GGACGGTGGC 120	
35	TGGCGGCAGA GACCCGCGGG AGCCCCCAGC G ATG TCG CGC CTG TTC CTC GCC 172	
	Met Ser Arg Leu Phe Leu Ala 1 5	
40	TGC CTG CTG GCC ATC TTC CCA GTG GTC TCC ATG AAG AGT CCC ATC TTC 220	
	Cys Leu Leu Ala Ile Phe Pro Val Val Ser Met Lys Ser Pro Ile Phe 10 15 20	
45	GGT CCC GAG GAG GTG AGC AGC GTG GAA GGC CGC TCA GTG TCC ATC AAG 268	
	Gly Pro Glu Glu Val Ser Ser Val Glu Gly Arg Ser Val Ser Ile Lys 25 30 35	
50	TGC TAC TAC CCG CCC ACC TCC GTC AAC CGG CAC ACG CGC AAG TAC TGG 316	
	Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp 40 45 50 55	
55	TGC CGG CAG GGA GCC CAG GGC CGC TGC ACG ACC CTC ATC TCC TCG GAG 364	
	Cys Arg Gln Gly Ala Gln Gly Arg Cys Thr Thr Leu Ile Ser Ser Glu 60 65 70	
60	GGC TAC GTC TCC GAC GAC TAC GTG GGC AGA GCC AAC CTC ACC AAC TTC 412	
	Gly Tyr Val Ser Asp Asp Tyr Val Gly Arg Ala Asn Leu Thr Asn Phe 75 80 85	
65	CCG GAG AGC GGC ACG TTT GTG GTG GAC ATC AGC CAT CTC ACC CAT AAA 460	
	Pro Glu Ser Gly Thr Phe Val Val Asp Ile Ser His Leu Thr His Lys 90 95 100	
	GAC TCA GGG CGC TAC AAG TGT GGC CTG GGC ATT AGC AGC CGT GGC CTT 508	
	Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile Ser Ser Arg Gly Leu 105 110 115	

	AAC TTC GAT GTG AGC CTG GAG GTC AGC CAA GAT CCT GCA CAG GCA AGT Asn Phe Asp Val Ser Leu Glu Val Ser Gln Asp Pro Ala Gln Ala Ser 120 125 130 135	556
5	CAT GCC CAC GTC TAC ACT ATA GAC CTG GGC AGG ACT GTG ACC ATC AAC His Ala His Val Tyr Thr Ile Asp Leu Gly Arg Thr Val Thr Ile Asn 140 145 150	604
10	TGC CCT TTC ACG CGT GCG AAT TCT GAG AAG AGA AAA TCC TTG TGC AAG Cys Pro Phe Thr Arg Ala Asn Ser Glu Lys Arg Lys Ser Leu Cys Lys 155 160 165	652
15	AAG ACA ATC CAG GAC TGT TTC CAA GTT GTC GAC TCC ACC GGG TAT GTG Lys Thr Ile Gln Asp Cys Phe Gln Val Val Asp Ser Thr Gly Tyr Val 170 175 180	700
20	AGC AAC AGC TAT AAA GAC AGA GCA CAT ATC AGT ATC CTA GGT ACC AAC Ser Asn Ser Tyr Lys Asp Arg Ala His Ile Ser Ile Leu Gly Thr Asn 185 190 195	748
25	ACA TTA GTG TTC AGC GTT GTC ATC AAC CGA GTC AAG CTC AGT GAT GCT Thr Leu Val Phe Ser Val Val Ile Asn Arg Val Lys Leu Ser Asp Ala 200 205 210 215	796
30	GGG ATG TAT GTC TGC CAG GCT GGG GAC GAT GCC AAA GCC GAT AAA ATC Gly Met Tyr Val Cys Gln Ala Gly Asp Asp Ala Lys Ala Asp Lys Ile 220 225 230	844
35	AGC ATT GAC CTC CAG GTG CTG GAG CCT GAG CTC GAG CTG GTT TAT GGA Asn Ile Asp Leu Gln Val Leu Glu Pro Glu Pro Glu Leu Val Tyr Gly 235 240 245	892
40	GAC TTG AGG AGC TCG GTG ACC TTT GAC TGT TCC CTG GGC CCC GAG GTG Asp Leu Arg Ser Ser Val Thr Phe Asp Cys Ser Leu Gly Pro Glu Val 250 255 260	940
45	GCA AAT GTG CCC AAA TTT CTG TGC CAG AAG AAG AAT GGG GGA GCT TGC Ala Asn Val Pro Lys Phe Leu Cys Gln Lys Lys Asn Gly Gly Ala Cys 265 270 275	988
50	AAT GTA GTC ATC AAC ACG TTG GGG AAG AAG GCT CAG GAC TTC CAG GGC Asn Val Val Ile Asn Thr Leu Gly Lys Lys Ala Gln Asp Phe Gln Gly 280 285 290 295	1036
55	AGG ATC GTG TCC GTG CCC AAG GAC AAT GGT GTC TTC AGT GTG CAC ATT Arg Ile Val Ser Val Pro Lys Asp Asn Gly Val Phe Ser Val His Ile 300 305 310	1084
60	ACC AGC CTG AGG AAA GAG GAC GCA GGG CGC TAC GTG TGC GGG GCC CAG Thr Ser Leu Arg Lys Glu Asp Ala Gly Arg Tyr Val Cys Gly Ala Gln 315 320 325	1132
65	CCT GAG GGT GAG CCC CAG GAC GGC TGG CCT GTG CAG GCC TGG CAA CTC Pro Glu Gly Glu Pro Gln Asp Gly Trp Pro Val Gln Ala Trp Gln Leu 330 335 340	1180
70	TTC GTC AAT GAA GAG ACG GCA ATC CCC GCA AGC CCC TCC GTG GTG AAA Phe Val Asn Glu Glu Thr Ala Ile Pro Ala Ser Pro Ser Val Val Lys 345 350 355	1228
75	GGT GTG AGG GGA GGC TCT GTG ACT GTA TCT TGC CCC TAC AAC CCT AAG Gly Val Arg Gly Gly Ser Val Thr Val Ser Cys Pro Tyr Asn Pro Lys 360 365 370 375	1276
80	GAT GCC AAC AGC GCG AAG TAC TGG TGT CAC TGG GAA GAG GCT CAA AAC Asp Ala Asn Ser Ala Lys Tyr Trp Cys His Trp Glu Glu Ala Gln Asn	1324

	380	385	390	
	GGC CGC TGC CCG CGG CTG GTG GAG AGC CGG GGG CTG ATG AAG GAG CAG Gly Arg Cys Pro Arg Leu Val Glu Ser Arg Gly Leu Met Lys Glu Gln 395 400 405			1372
5	TAC GAG GGC AGG CTG GTG CTG CTC ACC GAG CCG GGC AAC GGC ACC TAC Tyr Glu Gly Arg Leu Val Leu Leu Thr Glu Pro Gly Asn Gly Thr Tyr 410 415 420			1420
10	ACC GTC ATC CTC AAC CAG CTC ACC GAT CAG GAC GCC GGC TTC TAC TGG Thr Val Ile Leu Asn Gln Leu Thr Asp Gln Asp Ala Gly Phe Tyr Trp 425 430 435			1468
15	TGC GTG ACC GAC GGC GAC ACG CGC TGG ATC TCC ACA GTG GAG CTC AAG Cys Val Thr Asp Gly Asp Thr Arg Trp Ile Ser Thr Val Glu Leu Lys 440 445 450 455			1516
20	GTT GTC CAA GGA GAA CCA AGC CTC AAG GTA CCC AAG AAC GTC ACG GCT Val Val Gln Gly Glu Pro Ser Leu Lys Val Pro Lys Asn Val Thr Ala 460 465 470			1564
25	TGG CTG GGA GAG CCC TTA AAG CTC TCC TGC CAC TTC CCC TGC AAA TTC Trp Leu Gly Glu Pro Leu Lys Leu Ser Cys His Phe Pro Cys Lys Phe 475 480 485			1612
30	TAC TCC TTT GAG AAG TAC TGG TGT AAG TGG AGC AAC AGA GGC TGC AGC Tyr Ser Phe Glu Lys Tyr Trp Cys Lys Trp Ser Asn Arg Gly Cys Ser 490 495 500			1660
35	GCC CTG CCC ACC CAG AAC GAC GGC CCC AGC CAG GCC TTT GTG AGC TGC Ala Leu Pro Thr Gln Asn Asp Gly Pro Ser Gln Ala Phe Val Ser Cys 505 510 515			1708
40	GAC CAG AAC AGC CAG GTC GTC TCC CTG AAC CTG GAC ACA GTC ACC AAG Asp Gln Asn Ser Gln Val Val Ser Leu Asn Leu Asp Thr Val Thr Lys 520 525 530 535			1756
45	GAG GAT GAA GGC TGG TAC TGG TGT GGA GTG AAG GAA GGC CCC CGA TAC Glu Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys Glu Gly Pro Arg Tyr 540 545 550			1804
50	GGG GAG ACG GCG GCT GTC TAC GTG GCA GTG GAG AGC AGG GTG AAG GGG Gly Glu Thr Ala Ala Val Tyr Val Ala Val Glu Ser Arg Val Lys Gly 555 560 565			1852
55	TCC CAA GGC AAG CAA GTG AAA GCT GCC CCT GCG GGG GCG GCA ATA Ser Gln Gly Ala Lys Gln Val Lys Ala Ala Pro Ala Gly Ala Ala Ile 570 575 580			1900
60	CAG TCG AGG GCC GGG GAG ATC CAG AAC AAA GCC CTT CTG GAC CCC AGC Gln Ser Arg Ala Gly Glu Ile Gln Asn Lys Ala Leu Leu Asp Pro Ser 585 590 595			1948
65	TTT TTC GCA AAG GAA AGT GTG AAG GAC GCT GCT GGT GGA CCC GGA GCA Phe Phe Ala Lys Glu Ser Val Lys Asp Ala Ala Gly Gly Pro Gly Ala 600 605 610 615			1996
65	CCT GCA GAT CCT GGC CGC CCT ACA GGA TAC AGC GGG AGC TCC AAA GCA Pro Ala Asp Pro Gly Arg Pro Thr Gly Tyr Ser Gly Ser Ser Lys Ala 620 625 630			2044
65	CTG GTC TCC ACC CTG GTG CCC CTG GCC CTG GTC CTG GTC GCA GGG GTC Leu Val Ser Thr Leu Val Pro Leu Ala Leu Val Leu Val Ala Gly Val 635 640 645			2092

	GTG GCG ATC GGG GTG GTC CGA GCC CGG CAC AGG AAG AAC GTC GAC CGG Val Ala Ile Gly Val Val Arg Ala Arg His Arg Lys Asn Val Asp Arg 650 655 660	2140
5	ATT TCA ATC AGG AGC TAC CGG ACA GAT ATC AGC ATG TCA GAC TTT GAG Ile Ser Ile Arg Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu 665 670 675	2188
10	AAC TCC AGG GAT TTT GAA GGA CGT GAC AAC ATG GGA GCC TCT CCA GAG Asn Ser Arg Asp Phe Glu Gly Arg Asp Asn Met Gly Ala Ser Pro Glu 680 685 690 695	2236
15	GCC CAA GAG ACG TCT CTC GGA GGG AAG GAC GAG TTT GCC ACC ACT ACC Ala Gln Glu Thr Ser Leu Gly Gly Lys Asp Glu Phe Ala Thr Thr Thr 700 705 710	2284
20	GAG GAC ACC GTG GAG AGC AAA GAA CCC AAG AAG GCA AAG AGG TCG TCC Glu Asp Thr Val Glu Ser Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser 715 720 725	2332
25	AAG GAG GAA GCC GAC GAG GCC TTC ACC ACC TTC CTC CTC CAG GCC AAA Lys Glu Glu Ala Asp Glu Ala Phe Thr Thr Phe Leu Leu Gln Ala Lys 730 735 740	2380
30	AAC CTG GCC TCC GCC GCA ACC CAG AAC GGC CCG ACA GAA GCC TAG ACGGAG Asn Leu Ala Ser Ala Ala Thr Gln Asn Gly Pro Thr Glu Ala 745 750 755	2431
35	CCCTGGCGC CCCTTCCCTC CGCACGTGGC AATCACGCTC CGAACATCACGC TGATCCTCAG GGCCCTCAGC TCGGGGGGCT CCACTGCCTG CACTCACACC CCGCCTAGGC TTCTCCTGTC TGTCTCAGA GGGTGTGCTG GTTCCTTCTT GGTGGCATCC AAGCCTGGCT TACTTGTTC AAGGTGTGGA GGAGAATTAA GATCGCAGAG GGGCCTCTCA GAAAGAAAAG GAGTGGGTGG GGAGACAACC GCAGAAAGGG GGCCATTCA CGCTTCCCTG TCCCCTTATT TGGGGATGTC	2491 2551 2611 2671 2731 2791
40	AGTGGAAATCC TCCCTTCCAC CCCATCTCTG CACCTCTCCA TCCCCACTCC ATTCCATCTT CTCTTCTTCT TTCCCTCATT AAAATGTGC ATTTGGTTAC TCACTAGATT CCAGGGACTC	2851 2911
45	TGCTAGACAC TGGGATAGGT AGGCCGCAAT CCCAGGCGGC AGCCTCCGC AAACATCAAG GAGCCCCTGG AGCCCACAGC ATCTCTTCAC GTGTACACTC ACTGACCTCT GCCTCTGCTG GGAGAAATCA TAAAGGGTCT GCAGCCCTGA GGCCTTAGGG ATTATGTAAC ACAGGCATAC ACACAAGGCA CCATCAACAC ATTCTTACCA TTTCACAGGT GAGAAAGCCG AGGTCCCTGAG	2971 3031 3091 3151
50	AGGTGGAGAG GTTGCTCAG AGTCAGCAAG TGAGATGTAC GAGTCTCAAG CTAAAGATT GACACCTGCT GTCCCTACAG GAGGGCCTCC TCTCTCCAGA TGAGACAGCA TTCCATAGGA AGGAGAAGAA AAATGTAAAT AAGACTGGTC TTTCACAGGC CCCACATCAG GGAAGATA CCTTTCCCTG TCTGTCACTC ACAGAGACCT AATAGGATAA GAGAATGGTC AACACTCAA	3211 3271 3331 3391
55	CCCCCGAATG TGAAGAGTTC TAAGTGGAAA GGGAGGAAAA AGGGGGGATT TGATGGTGC AGGGAGGGC TGATCTCAA AGAACTAAGG TTTAAGTTT TTTGTTTTT TTTTCCTTC	3451 3511
60	TTCTAAGCTC TGCACTTCAA CTAGCATCTA TGAGCTGGCA CTTGCTAACAA AATCAAAAT	3571

GTGAATTAAT TAATAATTAA AGACCATGAT TTCCTCCAAA AAAAAAAA AAAAAAAA

3630

5 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 757 amino acids
 (B) TYPE: amino acid
 (C) STRANNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Bovine Polyimmunoglobulin Receptor

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

	Met	Ser	Arg	Leu	Phe	Leu	Ala	Cys	Leu	Leu	Ala	Ile	Phe	Pro	Val	Val
	1					5				10					15	
20	Ser	Met	Lys	Ser	Pro	Ile	Phe	Gly	Pro	Glu	Glu	Val	Ser	Ser	Val	Glu
		20						25						30		
	Gly	Arg	Ser	Val	Ser	Ile	Lys	Cys	Tyr	Tyr	Pro	Pro	Thr	Ser	Val	Asn
			35					40					45			
25	Arg	His	Thr	Arg	Lys	Tyr	Trp	Cys	Arg	Gln	Gly	Ala	Gln	Gly	Arg	Cys
				50			55				60					
30	Thr	Thr	Leu	Ile	Ser	Ser	Glu	Gly	Tyr	Val	Ser	Asp	Asp	Tyr	Val	Gly
		65				70			75				80			
	Arg	Ala	Asn	Leu	Thr	Asn	Phe	Pro	Glu	Ser	Gly	Thr	Phe	Val	Val	Asp
			85					90					95			
35	Ile	Ser	His	Leu	Thr	His	Lys	Asp	Ser	Gly	Arg	Tyr	Lys	Cys	Gly	Leu
			100				105				110					
	Gly	Ile	Ser	Ser	Arg	Gly	Leu	Asn	Phe	Asp	Val	Ser	Leu	Glu	Val	Ser
			115				120				125					
40	Gln	Asp	Pro	Ala	Gln	Ala	Ser	His	Ala	His	Val	Tyr	Thr	Ile	Asp	Leu
			130				135			140						
	Gly	Arg	Thr	Val	Thr	Ile	Asn	Cys	Pro	Phe	Thr	Arg	Ala	Asn	Ser	Glu
45		145				150				155			160			
	Lys	Arg	Lys	Ser	Leu	Cys	Lys	Lys	Thr	Ile	Gln	Asp	Cys	Phe	Gln	Val
			165					170				175				
50	Val	Asp	Ser	Thr	Gly	Tyr	Val	Ser	Asn	Ser	Tyr	Lys	Asp	Arg	Ala	His
			180				185				190					
	Ile	Ser	Ile	Leu	Gly	Thr	Asn	Thr	Leu	Val	Phe	Ser	Val	Val	Ile	Asn
			195					200				205				
55	Arg	Val	Lys	Leu	Ser	Asp	Ala	Gly	Met	Tyr	Val	Cys	Gln	Ala	Gly	Asp
			210				215				220					
60	Asp	Ala	Lys	Ala	Asp	Lys	Ile	Asn	Ile	Asp	Leu	Gln	Val	Leu	Glu	Pro
		225				230				235			240			
	Glu	Pro	Glu	Leu	Val	Tyr	Gly	Asp	Leu	Arg	Ser	Ser	Val	Thr	Phe	Asp
			245				250			255						
65	Cys	Ser	Leu	Gly	Pro	Glu	Val	Ala	Asn	Val	Pro	Lys	Phe	Leu	Cys	Gln
			260				265			270						

Lys Lys Asn Gly Gly Ala Cys Asn Val Val Ile Asn Thr Leu Gly Lys
 275 280 285

5 Lys Ala Gln Asp Phe Gln Gly Arg Ile Val Ser Val Pro Lys Asp Asn
 290 295 300

Gly Val Phe Ser Val His Ile Thr Ser Leu Arg Lys Glu Asp Ala Gly
 305 310 315 320

10 Arg Tyr Val Cys Gly Ala Gln Pro Glu Gly Glu Pro Gln Asp Gly Trp
 325 330 335

Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Thr Ala Ile Pro
 340 345 350

15 Ala Ser Pro Ser Val Val Lys Gly Val Arg Gly Gly Ser Val Thr Val
 355 360 365

20 Ser Cys Pro Tyr Asn Pro Lys Asp Ala Asn Ser Ala Lys Tyr Trp Cys
 370 375 380

His Trp Glu Glu Ala Gln Asn Gly Arg Cys Pro Arg Leu Val Glu Ser
 385 390 395 400

25 Arg Gly Leu Met Lys Glu Gln Tyr Glu Gly Arg Leu Val Leu Leu Thr
 405 410 415

Glu Pro Gly Asn Gly Thr Tyr Thr Val Ile Leu Asn Gln Leu Thr Asp
 420 425 430

30 Gln Asp Ala Gly Phe Tyr Trp Cys Val Thr Asp Gly Asp Thr Arg Trp
 435 440 445

Ile Ser Thr Val Glu Leu Lys Val Val Gln Gly Glu Pro Ser Leu Lys
 450 455 460

Val Pro Lys Asn Val Thr Ala Trp Leu Gly Glu Pro Leu Lys Leu Ser
 465 470 475 480

40 Cys His Phe Pro Cys Lys Phe Tyr Ser Phe Glu Lys Tyr Trp Cys Lys
 485 490 495

Trp Ser Asn Arg Gly Cys Ser Ala Leu Pro Thr Gln Asn Asp Gly Pro
 500 505 510

45 Ser Gln Ala Phe Val Ser Cys Asp Gln Asn Ser Gln Val Val Ser Leu
 515 520 525

Asn Leu Asp Thr Val Thr Lys Glu Asp Glu Gly Trp Tyr Trp Cys Gly
 530 535 540

50 Val Lys Glu Gly Pro Arg Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala
 545 550 555 560

55 Val Glu Ser Arg Val Lys Gly Ser Gln Gly Ala Lys Gln Val Lys Ala
 565 570 575

Ala Pro Ala Gly Ala Ala Ile Gln Ser Arg Ala Gly Glu Ile Gln Asn
 580 585 590

60 Lys Ala Leu Leu Asp Pro Ser Phe Phe Ala Lys Glu Ser Val Lys Asp
 595 600 605

65 Ala Ala Gly Gly Pro Gly Ala Pro Ala Asp Pro Gly Arg Pro Thr Gly
 610 615 620

Tyr Ser Gly Ser Ser Lys Ala Leu Val Ser Thr Leu Val Pro Leu Ala
 625 630 635 640
 Leu Val Leu Val Ala Gly Val Val Ala Ile Gly Val Val Arg Ala Arg
 5 645 650 655
 His Arg Lys Asn Val Asp Arg Ile Ser Ile Arg Ser Tyr Arg Thr Asp
 660 665 670
 10 Ile Ser Met Ser Asp Phe Glu Asn Ser Arg Asp Phe Glu Gly Arg Asp
 675 680 685
 Asn Met Gly Ala Ser Pro Glu Ala Gln Glu Thr Ser Leu Gly Gly Lys
 15 690 695 700
 Asp Glu Phe Ala Thr Thr Glu Asp Thr Val Glu Ser Lys Glu Pro
 705 710 715 720
 Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Glu Ala Phe Thr
 20 725 730 735
 Thr Phe Leu Leu Gln Ala Lys Asn Leu Ala Ser Ala Ala Thr Gln Asn
 740 745 750
 25 Gly Pro Thr Glu Ala
 755

30

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 3095 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 40 DESCRIPTION: Mouse Polyimmunoglobulin Receptor

(ix) FEATURE:

45 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 85....2400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

50	TCACCTGGAG AGAAGGAAGT AGCTAAAACA TTCTCATACA AGAACCAAC CTGAGCGGCA	60
	CAGCCCCCCT GGAAGCCACA AGCA ATG AGG CTC TAC TTG TTC ACG CTC TTG	
	Met Arg Leu Tyr Leu Phe Thr Leu Leu	
	1 5	
55	GTA ACT GTC TTT TCA GGG GTC TCC ACA AAA AGC CCC ATA TTT GGT CCC	159
10	Val Thr Val Phe Ser Gly Val Ser Thr Lys Ser Pro Ile Phe Gly Pro	
	15 20 25	
60	CAG GAG GTG AGT AGT ATA GAA GGC GAC TCT GTT TCC ATC ACG TGC TAC	207
	Gln Glu Val Ser Ser Ile Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr	
	30 35 40	
65	TAC CCA GAC ACC TCT GTC AAC CGG CAC ACC CGG AAA TAC TGG TGC CGA	255
	Tyr Pro Asp Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp Cys Arg	
	45 50 55	

	CAA GGA GCC AGC GGC ATG TGC ACA ACG CTC ATC TCT TCA AAT GGC TAC Gln Gly Ala Ser Gly Met Cys Thr Thr Leu Ile Ser Ser Asn Gly Tyr 60 65 70	303
5	CTC TCC AAG GAG TAT TCA GGC AGA GCC AAC CTC ATC AAC TTC CCA GAG Leu Ser Lys Glu Tyr Ser Gly Arg Ala Asn Leu Ile Asn Phe Pro Glu 75 80 85	351
10	AAC AAC ACA TTT GTG ATT AAC ATT GAG CAG CTC ACC CAG GAC GAC ACT Asn Asn Thr Phe Val Ile Asn Ile Glu Gln Leu Thr Gln Asp Asp Thr 90 95 100 105	399
15	GGG AGC TAC AAG TGT GGC CTG GGT ACC AGT AAC CGA GGC CTG TCC TTC Gly Ser Tyr Lys Cys Gly Leu Gly Thr Ser Asn Arg Gly Leu Ser Phe 110 115 120	447
20	GAT GTC AGC CTG GAG GTC AGC CAG GTT CCT GAG TTG CCG AGT GAC ACC Asp Val Ser Leu Glu Val Ser Gln Val Pro Glu Leu Pro Ser Asp Thr 125 130 135	495
25	CAC GTC TAC ACA AAG GAC ATA GGC AGA AAT GTG ACC ATT GAA TGC CCT His Val Tyr Thr Lys Asp Ile Gly Arg Asn Val Thr Ile Glu Cys Pro 140 145 150	543
30	TTC AAA AGG GAG AAT GTT CCC AGC AAG AAA TCC CTG TGT AAG AAG ACA Phe Lys Arg Glu Asn Val Pro Ser Lys Ser Leu Cys Lys Lys Thr 155 160 165	591
35	AAC CAG TCC TGC GAA CTT GTC ATT GAC TCT ACT GAG AAG GTG AAC CCC Asn Gln Ser Cys Glu Leu Val Ile Asp Ser Thr Glu Lys Val Asn Pro 170 175 180 185	639
40	AGC TAT ATA GGC AGA GCA AAA CTT TTT ATG AAA GGG ACC GAC CTA ACT Ser Tyr Ile Gly Arg Ala Lys Leu Phe Met Lys Gly Thr Asp Leu Thr 190 195 200	687
45	GTA TTC TAT GTC AAC ATT AGT CAC CTA ACG CAC AAT GAT GCT GGG CTG Val Phe Tyr Val Asn Ile Ser His Leu Thr His Asn Asp Ala Gly Leu 205 210 215	735
50	TAC ATC TGC CAA GCT GGA GAA GGT CCT AGT GCT GAT AAG AAG AAT GTT Tyr Ile Cys Gln Ala Gly Glu Gly Pro Ser Ala Asp Lys Lys Asn Val 220 225 230	783
55	GAC CTC CAG GTG CTA GCG CCT GAG CCA GAG CTG CTT TAT AAA GAC CTG Asp Leu Gln Val Leu Ala Pro Glu Pro Glu Leu Leu Tyr Lys Asp Leu 235 240 245	831
60	AGG TCC TCA GTG ACT TTT GAA TGT GAC CTG GGC CGT GAG GTG GCA AAC Arg Ser Ser Val Thr Phe Glu Cys Asp Leu Gly Arg Glu Val Ala Asn 250 255 260 265	879
65	GAG GCC AAA TAT CTG TGC CGG ATG AAT AAG GAA ACC TGT GAT GTG ATC Glu Ala Lys Tyr Leu Cys Arg Met Asn Lys Glu Thr Cys Asp Val Ile 270 275 280	927
	ATT AAC ACC CTG GGG AAG AGG GAT CCA GAC TTT GAG GGC AGG ATC CTG Ile Asn Thr Leu Gly Lys Arg Asp Pro Asp Phe Glu Gly Arg Ile Leu 285 290 295	975
	ATA ACC CCC AAG GAT GAC AAT GGC CGC TTC AGT GTG TTG ATC ACA GGC Ile Thr Pro Lys Asp Asp Asn Gly Arg Phe Ser Val Leu Ile Thr Gly 300 305 310	1023
	CTG AGG AAG GAG GAT GCA GGG CAC TAC CAG TGT GGA GCC CAC AGT TCT Leu Arg Lys Glu Asp Ala Gly His Tyr Gln Cys Gly Ala His Ser Ser	1071

	315	320	325	
5	GGT TTG CCT CAA GAA GGC TGG CCC ATC CAG ACT TGG CAA CTC TTT GTC Gly Leu Pro Gln Glu Gly Trp Pro Ile Gln Thr Trp Gln Leu Phe Val 330 335 340 345			1119
	AAT GAA GAG TCT ACC ATT CCC AAT CGT CGC TCT GTT GTG AAG GGA GTC Asn Glu Glu Ser Thr Ile Pro Asn Arg Arg Ser Val Val Lys Gly Val 350 355 360			1167
10	ACA GGA GGC TCT GTG GCC ATC GCC TGT CCC TAT AAC CCC AAG GAA AGC Thr Gly Gly Ser Val Ala Ile Ala Cys Pro Tyr Asn Pro Lys Glu Ser 365 370 375			1215
15	AGC AGC CTC AAG TAC TGG TGT CGC TGG GAA GGG GAC GGA AAT GGA CAT Ser Ser Leu Lys Tyr Trp Cys Arg Trp Glu Gly Asp Gly Asn Gly His 380 385 390			1263
20	TGC CCC GCG CTT GTG GGG ACC CAG GCC CAG GTG CAA GAA GAG TAT GAA Cys Pro Ala Leu Val Gly Thr Gln Ala Gln Val Gln Glu Glu Tyr Glu 395 400 405			1311
	GGC CGA CTG GCA CTG TTT GAT CAG CCA GGC AAT GGT ACT TAC ACT GTC Gly Arg Leu Ala Leu Phe Asp Gln Pro Gly Asn Gly Thr Tyr Thr Val 410 415 420 425			1359
25	ATC CTC AAC CAG CTC ACC ACC GAG GAT GCT GGC TTC TAT TGG TGT CTT Ile Leu Asn Gln Leu Thr Thr Glu Asp Ala Gly Phe Tyr Trp Cys Leu 430 435 440			1407
30	ACC AAT GGT GAC TCT CGC TGG AGA ACC ACA ATA GAA CTC CAG GTT GCC Thr Asn Gly Asp Ser Arg Trp Arg Thr Thr Ile Glu Leu Gln Val Ala 445 450 455			1455
35	GAA GCT ACA AGG GAG CCA AAC CTT GAG GTG ACG CCA CAG AAC GCA ACA Glu Ala Thr Arg Glu Pro Asn Leu Glu Val Thr Pro Gln Asn Ala Thr 460 465 470			1503
40	GCA GTA CTA GGA GAG ACC TTC ACC GTT TCC TGC CAC TAT CCG TGC AAA Ala Val Leu Gly Glu Thr Phe Thr Val Ser Cys His Tyr Pro Cys Lys 475 480 485			1551
	TTC TAC TCC CAG GAG AAA TAC TGG TGC AAG TGG AGC AAC AAG GGT TGC Phe Tyr Ser Gln Glu Lys Tyr Trp Cys Lys Trp Ser Asn Lys Gly Cys 490 495 500 505			1599
45	CAC ATC CTG CCA AGC CAT GAC GAA GGT GCC CGC CAA TCT TCT GTG AGC His Ile Leu Pro Ser His Asp Glu Gly Ala Arg Gln Ser Ser Val Ser 510 515 520			1647
50	TGC GAC CAG AGC AGC CAG CTG GTC TCC ATG ACC CTG AAC CCG GTC AGT Cys Asp Gln Ser Ser Gln Leu Val Ser Met Thr Leu Asn Pro Val Ser 525 530 535			1695
55	AAG GAA GAT GAA GGC TGG TAC TGG TGT GGG GTA AAG CAA GGC CAG ACC Lys Glu Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys Gln Gly Gln Thr 540 545 550			1743
60	TAT GGA GAA ACT ACC GCC ATC TAT ATA GCA GTT GAA GAG AGG ACC AGA Tyr Gly Glu Thr Thr Ala Ile Tyr Ile Ala Val Glu Glu Arg Thr Arg 555 560 565			1791
	GGG TCA TCC CAT GTC AAC CCA ACA GAT GCA AAT GCA CGT GCC AAA GTC Gly Ser Ser His Val Asn Pro Thr Asp Ala Asn Ala Arg Ala Lys Val			1839
65	570 575 580 585			

	GCT CTG GAA GAA GAG GTA GTG GAC TCC TCC ATC AGT GAA AAA GAG AAC Ala Leu Glu Glu Val Val Asp Ser Ser Ile Ser Glu Lys Glu Asn 590 595 600	1887
5	AAA GCC ATT CCA AAT CCC GGG CCT TTT GCC AAC GAA AGA GAG ATA CAG Lys Ala Ile Pro Asn Pro Gly Pro Phe Ala Asn Glu Arg Glu Ile Gln 605 610 615	1935
10	AAT GTG AGA GAC CAA GCT CAG GAG AAC AGA GCA TCT GGG GAT GCT GGC Asn Val Arg Asp Gln Ala Gln Glu Asn Arg Ala Ser Gly Asp Ala Gly 620 625 630	1983
15	AGT GCT GAT GGA CAA AGC AGG AGC TCC AGC TCC AAA GTG CTG TTC TCC Ser Ala Asp Gly Gln Ser Arg Ser Ser Ser Lys Val Leu Phe Ser 635 640 645	2031
20	ACC CTG GTG CCC CTG GGT CTG GTG CTG GCA GTG GGT GCT ATA GCT GTG Thr Leu Val Pro Leu Gly Leu Val Leu Ala Val Gly Ala Ile Ala Val 650 655 660 665	2079
25	TGG GTG GCC AGA GTC CGA CAT CGG AAG AAT GTA GAC CGC ATG TCA ATC Trp Val Ala Arg Val Arg His Arg Lys Asn Val Asp Arg Met Ser Ile 670 675 680	2127
30	AGC AGC TAC AGG ACA GAC ATT AGC ATG GCA GAC TTC AAG AAC TCC AGA Ser Ser Tyr Arg Thr Asp Ile Ser Met Ala Asp Phe Lys Asn Ser Arg 685 690 695	2175
35	GAT TTG GGA GGC AAT GAC AAC ATG GGG GCC TCT CCA GAC ACA CAG CAA Asp Leu Gly Gly Asn Asp Asn Met Gly Ala Ser Pro Asp Thr Gln Gln 700 705 710	2223
40	ACA GTC ATC GAA GGA AAA GAT GAA ATC GTG ACT ACC ACG GAG TGC ACC Thr Val Ile Glu Gly Lys Asp Glu Ile Val Thr Thr Glu Cys Thr 715 720 725	2271
45	GCT GAG CCA GAA GAA TCC AAG AAA GCA AAA AGG TCA TCC AAG GAG GAA Ala Glu Pro Glu Glu Ser Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu 730 735 740 745	2319
50	GCT GAC ATG GCC TAC TCG GCA TTC CTG CTT CAG TCC AGC ACC ATA GCT Ala Asp Met Ala Tyr Ser Ala Phe Leu Leu Gln Ser Ser Thr Ile Ala 750 755 760	2367
55	GCA CAG GTC CAC GAT GGT CCC CAG GAA GCC TAG GCAGTGCTGA CCACCCACCC Ala Gln Val His Asp Gly Pro Gln Glu Ala 765 770	2420
60	TTGCCTGTGA CAATCAACTT GAGAATCACA CTGATCCGCT CGCAGCCCAC ACTCACCCAT CACCTCCGCT CTTCCCTCCT GTCCTCAGAG GTGTGCTGGT TCCTTCCTCG GCCATGGAAG CCTGGCCTAG TTACGCCGT TTAGGAGAGA GTGTGAGGCG TTCTTTCTC TATGAAGAGA ATGTCAGCGT AACTCTTCTC TCCTCCATCT CTCCCTTCCT ATCCTCTTGA TTCAAACAAAC ACATCTGAGA ACTCACTAGG CTTCAGTGCC TACTAAATGC TGAGAGCCAG GCCACAATCT TTCTATAAAT ATTACTGGAA GAGATGCCAT CTCCCTCCAG ATTCTGTCTT TTCATTAAGA 65 TAAGACATCA TTACCAGGCA TACCTCCTGC CTCTGTGCCT CATAGGCATA CACAAGCCAT	2480 2540 2600 2660 2720 2780 2840 2900 2960

AAGGGCATCA TGATTTCACTGAGAAGAG ATGTTCTCA AGAGTGCCTA GTGAGATAGA 3020
CTAGCGTCAA ACCAGATGTG GCAACTCCTG GCTCTGGCC TACGATCTGT CTTCAAGAAA 3080
5 AAAAAAAAAA AAAAAA 3095

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Arg Leu Tyr Leu Phe Thr Leu Leu Val Thr Val Phe Ser Gly Val
 1 5 10 15

25 Ser Thr Lys Ser Pro Ile Phe Gly Pro Gln Glu Val Ser Ser Ile Glu
20 25 30

Gly Asp Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn
35 40 45

30 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Ser Gly Met Cys
50 55 60

Thr Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly
65 70 75 80

Arg Ala Asn Leu Ile Asn Phe Pro Glu Asn Asn Thr Phe Val Ile Asn
85 90 95

40 Ile Glu Gln Leu Thr Gln Asp Asp Thr Gly Ser Tyr Lys Cys Gly Leu
100 105 110

Gly Thr Ser Asn Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser
115 120 125

45 Gln Val Pro Glu Leu Pro Ser Asp Thr His Val Tyr Thr Lys Asp Ile
130 135 140

Gly Arg Asn Val Thr Ile Glu Cys Pro Phe Lys Arg Glu Asn Val Pro
145 150 155 160

Ser Lys Lys Ser Leu Cys Lys Lys Thr Asn Gln Ser Cys Glu Leu Val
165 170 175

55 Ile Asp Ser Thr Glu Lys Val Asn Pro Ser Tyr Ile Gly Arg Ala Lys
180 185 190

Lys Tyr Met Lys Gly Thr Asp Leu Thr Val Phe Tyr Val Asn Ile Ser
195 200 205

80 His Led The His Ash Asp Aia Gey Bed Tyr The Sys Gia And Gia
210 215 220

Gly P10 Ser Ala Asp Lys Lys Asn Val Asp Leu Glu Val Asp Ala Phe
225 230 235 240

Glu P10 Glu Ser Lys Tyr Lys Asp Ser Arg Ser Ser Val Thr Ile Ser

	245	250	255
	Cys Asp Leu Gly Arg Glu Val Ala Asn Glu Ala Lys Tyr Leu Cys Arg		
5	260	265	270
	Met Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr Leu Gly Lys Arg		
	275	280	285
10	Asp Pro Asp Phe Glu Gly Arg Ile Leu Ile Thr Pro Lys Asp Asp Asn		
	290	295	300
	Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly		
	305	310	315
	320		
15	His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro Gln Glu Gly Trp		
	325	330	335
	Pro Ile Gln Thr Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro		
20	340	345	350
	Asn Arg Arg Ser Val Val Lys Gly Val Thr Gly Gly Ser Val Ala Ile		
	355	360	365
25	Ala Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu Lys Tyr Trp Cys		
	370	375	380
	Arg Trp Glu Gly Asp Gly Asn Gly His Cys Pro Ala Leu Val Gly Thr		
	385	390	395
	400		
30	Gln Ala Gln Val Gln Glu Glu Tyr Glu Gly Arg Leu Ala Leu Phe Asp		
	405	410	415
	Gln Pro Gly Asn Gly Thr Tyr Thr Val Ile Leu Asn Gln Leu Thr Thr		
35	420	425	430
	Glu Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Ser Arg Trp		
	435	440	445
40	Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr Arg Glu Pro Asn		
	450	455	460
	Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Leu Gly Glu Thr Phe		
	465	470	475
	480		
45	Thr Val Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser Gln Glu Lys Tyr		
	485	490	495
	Trp Cys Lys Trp Ser Asn Lys Gly Cys His Ile Leu Pro Ser His Asp		
50	500	505	510
	Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln Ser Ser Gln Leu		
	515	520	525
	Val Ser Met Thr Leu Asn Pro Val Ser Lys Glu Asp Glu Gly Trp Tyr		
55	530	535	540
	Trp Cys Gly Val Lys Gln Gly Gln Thr Tyr Gly Glu Thr Thr Ala Ile		
	545	550	555
	560		
60	Tyr Ile Ala Val Glu Glu Arg Thr Arg Gly Ser Ser His Val Asn Pro		
	565	570	575
	Thr Asp Ala Asn Ala Arg Ala Lys Val Ala Leu Glu Glu Val Val		
	580	585	590
65	Asp Ser Ser Ile Ser Glu Lys Glu Asn Lys Ala Ile Pro Asn Pro Gly		

	595	600	605
5	Pro Phe Ala Asn Glu Arg Glu Ile Gln Asn Val Arg Asp Gln Ala Gln 610 615 620		
10	Glu Asn Arg Ala Ser Gly Asp Ala Gly Ser Ala Asp Gly Gln Ser Arg 625 630 635 640		
15	Ser Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu 645 650 655		
20	Val Leu Ala Val Gly Ala Ile Ala Val Trp Val Ala Arg Val Arg His 660 665 670		
25	Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile 675 680 685		
30	Ser Met Ala Asp Phe Lys Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn 690 695 700		
35	Met Gly Ala Ser Pro Asp Thr Gln Gln Thr Val Ile Glu Gly Lys Asp 705 710 715 720		
40	Glu Ile Val Thr Thr Glu Cys Thr Ala Glu Pro Glu Glu Ser Lys 725 730 735		
45	Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala 740 745 750		
50	Phe Leu Leu Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro 755 760 765		
55	Gln Glu Ala 770		

(2) INFORMATION FOR SEQ ID NO: 9:

40 (i) SEQUENCE CHARACTERISTICS:

45	(A) LENGTH: 3269 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	DESCRIPTION: Rat Polyimmunoglobulin Receptor

(ix) FEATURE:

50	(A) NAME/KEY: Coding Sequence
	(B) LOCATION: 74....2383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

55	GGCAACGAAG GTACCATGGA TCTTATACAA GAAGTGAACC AACATGCCGC AACCTCCTTG	60
	GAAGCCACAA GCG ATG AGG CTC TCC TTG TTC GCC CTC TTG GTA ACT GTC	109
	Met Arg Leu Ser Leu Phe Ala Leu Leu Val Thr Val	
60	1 5 10	
	TTC TCA GGG GTC TCC ACA CAA AGC CCC ATA TTT GGT CCC CAG GAT GTG	157
	Phe Ser Gly Val Ser Thr Gln Ser Pro Ile Phe Gly Pro Gln Asp Val	
	15 20 25	
65	AGT AGT ATT GAA GGT AAC TCG GTC TCC ATC ACG TGC TAC TAC CCA GAC	205
	Ser Ser Ile Glu Gly Asn Ser Val Ile Thr Cys Tyr Tyr Pro Asp	

	30	35	40	
5	ACC TCT GTC AAC CGG CAC ACC CGG AAA TAC TGG TGC CGA CAA GGA GCC Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala 45 50 55 60			253
10	AAC GGC TAC TGC GCA ACC CTC ATC TCT TCA AAT GGC TAC CTC TCG AAG Asn Gly Tyr Cys Ala Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys 65 70 75			301
15	GAG TAT TCA GGC AGA GCC AGC CTC ATC AAC TTC CCA GAG AAT AGC ACA Glu Tyr Ser Gly Arg Ala Ser Leu Ile Asn Phe Pro Glu Asn Ser Thr 80 85 90			349
20	TTT GTG ATT AAC ATT GCA CAT CTC ACC CAG GAG GAC ACT GGG AGC TAC Phe Val Ile Asn Ile Ala His Leu Thr Gln Glu Asp Thr Gly Ser Tyr 95 100 105			397
25	AAG TGT GGT CTG GGT ACC ACT AAC CGA GGC CTG TTT TTC GAT GTC AGC Lys Cys Gly Leu Gly Thr Thr Asn Arg Gly Leu Phe Phe Asp Val Ser 110 115 120			445
30	CTG GAG GTC AGC CAG GTT CCT GAG TTC CCA AAT GAC ACC CAT GTC TAC Leu Glu Val Ser Gln Val Pro Glu Phe Pro Asn Asp Thr His Val Tyr 125 130 135 140			493
35	ACA AAG GAC ATA GGC AGA ACT GTG ACC ATC GAA TGC CGT TTC AAA GAG Thr Lys Asp Ile Gly Arg Thr Val Thr Ile Glu Cys Arg Phe Lys Glu 145 150 155			541
40	GGG AAT GCT CAT AGC AAG AAA TCC CTG TGT AAG AAG AGA GGA GAG GCC Gly Asn Ala His Ser Lys Ser Leu Cys Lys Arg Gly Glu Ala 160 165 170			589
45	TGC GAA GTT GTC ATC GAC TCT ACT GAG TAC GTG GAC CCC AGC TAT AAG Cys Glu Val Val Ile Asp Ser Thr Glu Tyr Val Asp Pro Ser Tyr Lys 175 180 185			637
50	GAC AGA GCA ATC CTT TTT ATG AAA GGG ACC AGC CGC GAT ATA TTC TAT Asp Arg Ala Ile Leu Phe Met Lys Gly Thr Ser Arg Asp Ile Phe Tyr 190 195 200			685
55	GTC AAC ATT AGC CAC CTA ATA CCC AGT GAT GCT GGA CTG TAT GTT TGC Val Asn Ile Ser His Leu Ile Pro Ser Asp Ala Gly Leu Tyr Val Cys 205 210 215 220			733
60	CAA GCT GGA GAA GGC CCC AGT GCT GAT AAA AAT AAT GCT GAC CTC CAG Gln Ala Gly Glu Gly Pro Ser Ala Asp Lys Asn Asn Ala Asp Leu Gln 225 230 235			781
65	GTG CTA GAG CCT GAG CCA GAG CTG CTT TAT AAA GAC CTG AGG TCC TCA Val Leu Glu Pro Glu Pro Leu Leu Tyr Lys Asp Leu Arg Ser Ser 240 245 250			829
70	GTG ACT TTT GAA TGT GAC CTG GGC CGT GAA GTG GCA AAT GAT GCC AAA Val Thr Phe Glu Cys Asp Leu Gly Arg Glu Val Ala Asn Asp Ala Lys 255 260 265			877
75	TAT CTG TGT CGG AAG AAC AAG GAA ACC TGT GAT GTC ATC ATC AAC ACC Tyr Leu Cys Arg Lys Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr 270 275 280			925
80	CTG GGG AAG AGA GAT CCA GCC TTT GAA GGC AGG ATC CTG CTA ACC CCC Leu Gly Lys Arg Asp Pro Ala Phe Glu Gly Arg Ile Leu Leu Thr Pro 285 290 295 300			973

	AGG GAT GAC AAT GGC CGC TTC AGT GTG TTG ATC ACA GGC CTG AGG AAG Arg Asp Asp Asn Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys 305 310 315	1021
5	GAG GAT GCA GGG CAC TAC CAG TGT GGA GCG CAC AGT TCT GGT TTG CCT. Glu Asp Ala Gly His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro 320 325 330	1069
10	CAA GAA GGC TGG CCC GTC CAG GCT TGG CAA CTC TTT GTC AAT GAA GAG Gln Glu Gly Trp Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu 335 340 345	1117
15	TCC ACG ATT CCC AAT AGT CGC TCT GTT GTG AAG GGT GTC ACA GGA GGC Ser Thr Ile Pro Asn Ser Arg Ser Val Val Lys Gly Val Thr Gly Gly 350 355 360	1165
20	TCT GTG GCC ATC GTC TGT CCC TAT AAC CCC AAG GAA AGC AGC AGC CTC Ser Val Ala Ile Val Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu 365 370 375 380	1213
	AAG TAC TGG TGT CAC TGG GAA GCC GAC GAG AAT GGA CGC TGC CCG GTG Lys Tyr Trp Cys His Trp Glu Ala Asp Glu Asn Gly Arg Cys Pro Val 385 390 395	1261
25	CTC GTG GGG ACC CAG GCC CTG GTG CAA GAA GGA TAT GAA GGC CGA CTG Leu Val Gly Thr Gln Ala Leu Val Gln Glu Gly Tyr Glu Gly Arg Leu 400 405 410	1309
30	GCA CTG TTC GAT CAG CCG GGC AGT GGC GCC TAC ACT GTC ATC CTC AAC Ala Leu Phe Asp Gln Pro Gly Ser Gly Ala Tyr Thr Val Ile Leu Asn 415 420 425	1357
35	CAG CTC ACC ACC CAG GAT TCT GGC TTC TAC TGG TGT CTT ACC GAT GGT Gln Leu Thr Thr Gln Asp Ser Gly Phe Tyr Trp Cys Leu Thr Asp Gly 430 435 440	1405
40	GAC TCT CGC TGG AGA ACC ACG ATA GAA CTG CAG GTT GCT GAA GCT ACA Asp Ser Arg Trp Arg Thr Ile Glu Leu Gln Val Ala Glu Ala Thr 445 450 455 460	1453
	AAG AAG CCA GAC CTT GAG GTG ACA CCA CAG AAC GCG ACC GCG GTG ATA Lys Lys Pro Asp Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Ile 465 470 475	1501
45	GGA GAG ACC TTC ACA ATC TCC TGC CAC TAT CCG TGC AAA TTC TAC TCC Gly Glu Thr Phe Thr Ile Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser 480 485 490	1549
50	CAG GAG AAA TAC TGG TGC AAG TGG AGC AAC GAC GGC TGC CAC ATC CTG Gln Glu Lys Tyr Trp Cys Lys Trp Ser Asn Asp Gly Cys His Ile Leu 495 500 505	1597
55	CCG AGC CAT GAT GAA GGT GCC CGC CAG TCC TCT GTG AGC TGT GAC CAG Pro Ser His Asp Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln 510 515 520	1645
60	AGC AGC CAG ATC GTC TCC ATG ACC CTG AAC CCG GTC AAA AAG GAA GAT Ser Ser Gln Ile Val Ser Met Thr Leu Asn Pro Val Lys Lys Glu Asp 525 530 535 540	1693
	GAA GGC TGG TAC TGG TGT GGG GTA AAA GAA GGT CAG GTC TAT GGA GAA Glu Gly Trp Tyr Trp Cys Gly Val Lys Glu Gly Gln Val Tyr Gly Glu 545 550 555	1741
65	ACT ACA GCC ATC TAT GTA GCA GTT GAA GAG AGG ACC AGA GGG TCA CCC Thr Thr Ala Ile Tyr Val Ala Val Glu Glu Arg Thr Arg Gly Ser Pro	1789

	560	565	570	
5	CAC ATC AAC CCG ACA GAT GCA AAC GCA CGT GCA AAA GAT GCT CCA GAG His Ile Asn Pro Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu 575 580 585			1837
10	GAA GAG GCA ATG GAA TCC TCT GTC AGG GAG GAT GAA AAC AAG GCC AAT Glu Glu Ala Met Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn 590 595 600			1885
15	CTG GAC CCC AGG CTT TTT GCA GAC GAA AGA GAG ATA CAG AAT GCG GGA Leu Asp Pro Arg Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly 605 610 615 620			1933
20	GAC CAA GCT CAG GAG AAC AGA GCA TCT GGG AAT GCT GGC AGT GCT GGT Asp Gln Ala Gln Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly 625 630 635			1981
25	GGA CAA AGC GGG AGC TCC AAA GTC CTA TTC TCC ACC CTG GTG CCC CTG Gly Gln Ser Gly Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu 640 645 650			2029
30	GGT TTG GTG CTG GCA GTG GGT GCT GTG GCT GTG TGG GTG GCC AGA GTC Gly Leu Val Leu Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val 655 660 665			2077
35	CGA CAT CGG AAG AAT GTA GAC CGC ATG TCA ATC AGC AGC TAC AGG ACA Arg His Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr 670 675 680			2125
40	GAC ATT AGC ATG GGA GAC TTC AGG AAC TCC AGG GAT TTG GGA GGC AAT Asp Ile Ser Met Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn 685 690 695 700			2173
45	GAC AAC ATG GGC GCC ACT CCA GAC ACA CAA GAA ACA GTC CTC GAA GGA Asp Asn Met Gly Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly 705 710 715			2221
50	AAA GAT GAA ATA GAG ACT ACC ACC GAG TGT ACC ACC GAG CCA GAG GAA Lys Asp Glu Ile Glu Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu 720 725 730			2269
55	TCC AAG AAA GCA AAA AGG TCA TCC AAG GAG GAA GCT GAC ATG GCC TAC Ser Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr 735 740 745			2317
60	TCA GCA TTC CTG TTT CAG TCC AGC ACA ATA GCT GCG CAG GTC CAT GAT Ser Ala Phe Leu Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp 750 755 760			2365
65	GGT CCC CAG GAA GCC TAG GCAGTGCTGA CCACCTACCC CTGCCTGTGA CAATCAACT Gly Pro Gln Glu Ala 765			2422
70	TGAGAATCAC ATTGATCCAC TCGCAGCCCA CCCTCGCCCA TCACCCAGGC TCTTCCCTCC TGTCTCAGA GGTGTGCTGG TTCCTCCCTC AGTCGTGGAA GCCTGGCCTA CTTATGCCTG			2482
75	TTTAGGAGAG AGCGTGAGGA GTTCTTTTG CTGTTAAAGA GTAAGGTGGA AATGAGTTGA GCCCAAGAGG TGTCTCTGAG AGACGAGGGT TCAGAGCAGG GGCTCATTTC AGGAGGAAGA			2542
80	GCCATTTGAA GCCTCTTAT ACACATATGC TAGGATGTCA GGATAGCTCT TCTCCTCCAT			2602
85	CTCTCCTTTC TTCTCTTCTT GATTCAAGACA ACAGATCCGA AAACTCACTA GGCTTCCGGT			2662
90				2722
95				2782

	GTCTACTAAA TGCTGAGAGT CAGGCCACAG CCTTTCTATA AACATCACTG GAAGAGACAC	2842
	CACCTCGTCC CAGATTCTGT CTTTCCCTA AGCTATCAAT CATTACCGGG GATTCCCTT	2902
5	GCCTCTGCAC CTCATAGGCA ACAAAAGAAA CATAAGTCCT GCAGTCTAAG GCATACCAA	2962
	GCCATAAGGG CACCACGAGA CTCAGATGAG AAGAGATTT TCTCCAGAGT ACTCAGTGAG	3022
10	ATAGACTAGT GTCAAGCCAG ATGGGGCAAC TCCTGGCTCT TGGCCTGGGA CTTGTCTTCA	3082
	AGATCTCTGC TCTTATTAGA GAAAGAACTT TAGCATGAGG AAAACTAAGA GAAAACAAGT	3142
	TACATGGGCA TGGTGGTGTG CTCCCTGCAAT CCCAATATTA AGAGGTTAAA AAATAGGACC	3202
15	AGAAGTTAA AGTAATCCTT GGCTACCTAG TGAGTGTAAAG GCCAGCCTGG AATCAATAAG	3262
	AGTTGGT	3269

20

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH:	770 amino acids
	(B) TYPE:	amino acid
	(C) STRANNESS:	single
	(D) TOPOLOGY:	linear
	DESCRIPTION:	Rat Polyimmunoglobulin Receptor

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

	Met Arg Leu Ser Leu Phe Ala Leu Leu Val Thr Val Phe Ser Gly Val
	1 5 10 15
35	Ser Thr Gln Ser Pro Ile Phe Gly Pro Gln Asp Val Ser Ser Ile Glu
	20 25 30
	Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn
40	35 40 45
	Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Asn Gly Tyr Cys
	50 55 60
45	Ala Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly
	65 70 75 80
	Arg Ala Ser Leu Ile Asn Phe Pro Glu Asn Ser Thr Phe Val Ile Asn
	85 90 95
50	Ile Ala His Leu Thr Gln Glu Asp Thr Gly Ser Tyr Lys Cys Gly Leu
	100 105 110
	Gly Thr Thr Asn Arg Gly Leu Phe Phe Asp Val Ser Leu Glu Val Ser
55	115 120 125
	Gln Val Pro Glu Phe Pro Asn Asp Thr His Val Tyr Thr Lys Asp Ile
	130 135 140
60	Gly Arg Thr Val Thr Ile Glu Cys Arg Phe Lys Glu Gly Asn Ala His
	145 150 155 160
	Ser Lys Lys Ser Leu Cys Lys Lys Arg Gly Glu Ala Cys Glu Val Val
	165 170 175
65	Ile Asp Ser Thr Glu Tyr Val Asp Pro Ser Tyr Lys Asp Arg Ala Ile

	180	185	190
	Leu Phe Met Lys Gly Thr Ser Arg Asp Ile Phe Tyr Val Asn Ile Ser		
5	195	200	205
	His Leu Ile Pro Ser Asp Ala Gly Leu Tyr Val Cys Gln Ala Gly Glu		
	210	215	220
10	Gly Pro Ser Ala Asp Lys Asn Asn Ala Asp Leu Gln Val Leu Glu Pro		
	225	230	235
	Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser Val Thr Phe Glu		
	245	250	255
15	Cys Asp Leu Gly Arg Glu Val Ala Asn Asp Ala Lys Tyr Leu Cys Arg		
	260	265	270
	Lys Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr Leu Gly Lys Arg		
20	275	280	285
	Asp Pro Ala Phe Glu Gly Arg Ile Leu Leu Thr Pro Arg Asp Asp Asn		
	290	295	300
25	Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly		
	305	310	315
	His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro Gln Glu Gly Trp		
	325	330	335
30	Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro		
	340	345	350
35	Asn Ser Arg Ser Val Val Lys Gly Val Thr Gly Gly Ser Val Ala Ile		
	355	360	365
	Val Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu Lys Tyr Trp Cys		
	370	375	380
40	His Trp Glu Ala Asp Glu Asn Gly Arg Cys Pro Val Leu Val Gly Thr		
	385	390	395
	Gln Ala Leu Val Gln Glu Gly Tyr Glu Gly Arg Leu Ala Leu Phe Asp		
	405	410	415
45	Gln Pro Gly Ser Gly Ala Tyr Thr Val Ile Leu Asn Gln Leu Thr Thr		
	420	425	430
50	Gln Asp Ser Gly Phe Tyr Trp Cys Leu Thr Asp Gly Asp Ser Arg Trp		
	435	440	445
	Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr Lys Lys Pro Asp		
	450	455	460
55	Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Ile Gly Glu Thr Phe		
	465	470	475
	Thr Ile Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser Gln Glu Lys Tyr		
	485	490	495
60	Trp Cys Lys Trp Ser Asn Asp Gly Cys His Ile Leu Pro Ser His Asp		
	500	505	510
65	Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln Ser Ser Gln Ile		
	515	520	525

Val Ser Met Thr Leu Asn Pro Val Lys Lys Glu Asp Glu Gly Trp Tyr
 530 535 540
 Trp Cys Gly Val Lys Glu Gly Gln Val Tyr Gly Glu Thr Thr Ala Ile
 5 545 550 555 560
 Tyr Val Ala Val Glu Glu Arg Thr Arg Gly Ser Pro His Ile Asn Pro
 565 570 575
 10 Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu Glu Ala Met
 580 585 590
 Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn Leu Asp Pro Arg
 595 600 605
 15 Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly Asp Gln Ala Gln
 610 615 620
 Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly Gly Gln Ser Gly
 20 625 630 635 640
 Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu Val Leu
 645 650 655
 25 Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val Arg His Arg Lys
 660 665 670
 Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile Ser Met
 675 680 685
 30 Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn Met Gly
 690 695 700
 Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly Lys Asp Glu Ile
 35 705 710 715 720
 Glu Thr Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu Ser Lys Lys Ala
 725 730 735
 40 Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala Phe Leu
 740 745 750
 Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro Gln Glu
 755 760 765
 45 Ala

50 (2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Guy's 13 Kappa

60 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 8....320

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTCGAGC GAC ATT GTG ATG ACC CAG TCT CCA GCA ATC ATG TCT GCA TCT Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser 1 5 10	49
5 CCA GGG GAG AAG GTC ACC ATA ACC TGC AGT GCC AGC TCA AGT GTA AGT Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser 15 20 25 30	97
10 TAC ATG CAC TGG TTC CAG CAG AAG CCA GGC ACT TCT CCC AAA CTC TGG Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp 35 40 45	145
15 CTT TAT AGC ACA TCC AAC CTG GCT TCT GGA GTC CCT GCT CGC TTC AGT Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser 50 55 60	193
20 GGC AGT GGA TCT GGG ACC TCT TAC TCT CTC ACA ATC AGC CGA ATG GAG Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu 65 70 75	241
25 TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA A TA Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile 95 100 105	322
30 (2) INFORMATION FOR SEQ ID NO: 12: (i) SEQUENCE CHARACTERISTICS:	
35 (A) LENGTH: 105 amino acids (B) TYPE: amino acid (C) STRANDNESS: single (D) TOPOLOGY: linear DESCRIPTION: Guy's 13 Kappa	
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12: Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly 1 5 10 15	
45 Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met 20 25 30	
50 His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Leu Tyr 35 40 45	
55 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser 50 55 60	
60 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu 65 70 75 80	
65 Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Thr Ser Tyr Pro Tyr Thr 85 90 95	
65 (2) INFORMATION FOR SEQ ID NO: 13:	

(i) SEQUENCE CHARACTERISTICS:

10 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 7...402

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CTCGAG ATG GAA TGG ACC TGG GTT TTT CTC TTC CTC CTG TCA GGA ACT	48
Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Gly Thr	
1 5 10	
 GCA GGC GTC CAC TCT GGG GTC CAG CTT CAG CAG TCA GGA CCT GAC CTG	96
Ala Gly Val His Ser Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu	
15 20 25 30	
 GTG AAA CCT GGG GCC TCA GTG AAG ATA TCC TGC AAG GCT TCT GGA TAC	144
Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr	
35 40 45	
 ACA TTC ACT GAC TAC AAC ATA CAC TGG GTG AAG CAG AGC CGT GGA AAG	192
Thr Phe Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys	
50 55 60	
 AGC CTT GAG TGG ATT GGA TAT ATT TAT CCT TAC AAT GGT AAT ACT TAC	240
Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr	
65 70 75	
 TAC AAC CAG AAG TTC AAG AAC AAG GCC ACA TTG ACT GTA GAC AAT TCC	288
Tyr Asn Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser	
80 85 90	
 TCC ACC TCA GCC TAC ATG GAG CTC CGC AGC CTG ACA TCT GAG GAC TCT	336
Ser Thr Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser	
95 100 105 110	
 GCA GTC TAT TAC TGT GCA ACC TAC TTT GAC TAC TGG GGC CAA GGC ACC	384
Ala Val Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr	
115 120 125	
 ACT CTC ACA GTC TCC TCA	402
Thr Leu Thr Val Ser Ser	
130	

55 (2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1 5 10 15

5 Val His Ser Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys
 20 25 30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

10 Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys Ser Leu
 50 55 60

Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr Tyr Asn
 65 70 75 80

15 Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Thr
 85 90 95

Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 20 100 105 110

Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
 115 120 125

25 Thr Val Ser Ser
 130

30

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ACCAGATCTA TGGAATGGAC CTGGGTTTT C 31

45

50 (2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CCCAAGCTTG GTTTGGAGA TGGTTTCTC 30

65

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GATAAGCTTG GTCCTACTCC TCCTCCTCCT A 31

15 (2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AATCTCGAGT CAGTAGCAGA TGCCATCTCC 30

30

35 (2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGAAAGCTTT GTACATATGC AAGGCTTACA 30